

SCORE Search Results Details for Application 10519539 and Search Result us-10-519-539-127.rapbn.

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This page gives you Search Results detail for the Application 10519539 and Search Result us-10-519-539-127.rapbn.

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OM protein - protein search, using sw model

Run on: August 17, 2006, 15:33:26 ; Search time 33 Seconds
(without alignments)
67.754 Million cell updates/sec

Title: US-10-519-539-127
Perfect score: 159
Sequence: 1 GSR CIRRRISILFFVFRVLR SRRLRS AEIYES 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 243793 seqs, 67754213 residues

Total number of hits satisfying chosen parameters: 243793

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	53	33.3	825	7	US-11-330-403-16934	Sequence 16934, A
2	51	32.1	341	6	US-10-471-571A-2868	Sequence 2868, Ap
3	49.5	31.1	128	6	US-10-449-902-50000	Sequence 50000, A
4	48	30.2	707	6	US-10-449-902-53022	Sequence 53022, A
5	48	30.2	707	6	US-10-449-902-53218	Sequence 53218, A
6	47	29.6	367	6	US-10-953-349-29519	Sequence 29519, A
7	47	29.6	367	7	US-11-056-355B-69209	Sequence 69209, A
8	47	29.6	369	6	US-10-953-349-29518	Sequence 29518, A
9	47	29.6	369	7	US-11-056-355B-69208	Sequence 69208, A

10	47	29.6	421	6	US-10-953-349-29517	Sequence 29517, A
11	47	29.6	421	7	US-11-056-355B-69207	Sequence 69207, A
12	47	29.6	492	7	US-11-330-403-12587	Sequence 12587, A
13	46.5	29.2	967	6	US-10-449-902-52043	Sequence 52043, A
14	46.5	29.2	1037	7	US-11-051-725-100	Sequence 100, App
15	46.5	29.2	1463	7	US-11-051-725-104	Sequence 104, App
16	46.5	29.2	1481	7	US-11-051-725-17	Sequence 17, Appl
17	46.5	29.2	1966	6	US-10-829-000-5	Sequence 5, Appli
18	46.5	29.2	1966	6	US-10-829-000-6	Sequence 6, Appli
19	46.5	29.2	1977	6	US-10-829-000-7	Sequence 7, Appli
20	46	28.9	261	7	US-11-192-046-81	Sequence 81, Appl
21	46	28.9	297	7	US-11-192-046-213	Sequence 213, App
22	46	28.9	297	7	US-11-192-046-227	Sequence 227, App
23	46	28.9	297	7	US-11-192-046-241	Sequence 241, App
24	46	28.9	351	7	US-11-056-355B-11400	Sequence 11400, A
25	46	28.9	359	7	US-11-056-355B-11399	Sequence 11399, A
26	46	28.9	365	7	US-11-330-403-8917	Sequence 8917, Ap
27	46	28.9	371	7	US-11-056-355B-11398	Sequence 11398, A
28	45.5	28.6	299	7	US-11-051-725-156	Sequence 156, App
29	45.5	28.6	299	7	US-11-051-725-172	Sequence 172, App
30	45.5	28.6	500	7	US-11-051-725-140	Sequence 140, App
31	45.5	28.6	618	6	US-10-449-902-46626	Sequence 46626, A
32	45.5	28.6	695	7	US-11-051-725-184	Sequence 184, App
33	45.5	28.6	2105	7	US-11-051-725-9	Sequence 9, Appli
34	45.5	28.6	2123	7	US-11-051-725-180	Sequence 180, App
35	45.5	28.6	2152	7	US-11-051-725-22	Sequence 22, Appl
36	45.5	28.6	2161	6	US-10-829-000-4	Sequence 4, Appli
37	45.5	28.6	2161	7	US-11-051-725-188	Sequence 188, App
38	45.5	28.6	2169	7	US-11-051-725-5	Sequence 5, Appli
39	45.5	28.6	2182	7	US-11-051-725-8	Sequence 8, Appli
40	45.5	28.6	2192	7	US-11-051-725-147	Sequence 147, App
41	45.5	28.6	2221	6	US-10-829-000-3	Sequence 3, Appli
42	45.5	28.6	2221	7	US-11-051-725-162	Sequence 162, App
43	45	28.3	502	7	US-11-330-403-3929	Sequence 3929, Ap
44	45	28.3	513	7	US-11-330-403-1406	Sequence 1406, Ap
45	45	28.3	1226	6	US-10-530-117-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-11-330-403-16934
; Sequence 16934, Application US/11330403
; Publication No. US20060159563A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 16934
; LENGTH: 825
; TYPE: PRT
; ORGANISM: Psychrobacter sp. 273-4
US-11-330-403-16934

Query Match 33.3%; Score 53; DB 7; Length 825;
Best Local Similarity 39.3%; Pred. No. 6.7;
Matches 11; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 4 CIRRRISILFFVFRVLRSRRLRS AEIY 31
| : | : | | : | | | : |
Db 8 CLFCRHHLLFFAYRHLSIRSVMRKIPVY 35

RESULT 2

US-10-471-571A-2868
; Sequence 2868, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A

```
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 2868
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(341)
; OTHER INFORMATION: ABC transporter ATP-binding
US-10-471-571A-2868
```

```
Query Match          32.1%; Score 51; DB 6; Length 341;
Best Local Similarity 40.7%; Pred. No. 5.5;
Matches 11; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
```

```
Qy      1 GSR CIRRRISILFFVFRVLR SRRLRS 27
        | | |::|::| | :| || |::
Db      76 GLRAKRQKVS MIFQHFNLLWSRTVLKN 102
```

RESULT 3

```
US-10-449-902-50000
; Sequence 50000, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50000
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-50000
```

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Query Match          31.1%; Score 49.5; DB 6; Length 128;
Best Local Similarity 36.6%; Pred. No. 3.4;
Matches 15; Conservative 9; Mismatches 8; Indels 9; Gaps 3;
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```
Qy      2 SRCI----RRRISILF--FVFRVLR S---RRVLRSAEIYES 33
        |||: |||: | |:|::|:: | |: ||: |
Db      54 SRCVSPDLRRRLGFFFFSFIFQLLQNILLMRGWRAEEIFFS 94
```

RESULT 4

```
US-10-449-902-53022
; Sequence 53022, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53022
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53022
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```
Query Match          30.2%; Score 48; DB 6; Length 707;
Best Local Similarity 45.5%; Pred. No. 32;
Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      12 LFFVFRVLRSSRRVLRSAEYES 33
        ||| ||| || : ||: : ::
Db      220 LFFALRVLLSRSLRSSTVLQN 241
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RESULT 5

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US-10-449-902-53218
; Sequence 53218, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53218
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-53218
```

```
Query Match          30.2%; Score 48; DB 6; Length 707;
Best Local Similarity 45.5%; Pred. No. 32;
Matches 10; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      12 LFFVFRVLRSSRRVLRSAEYES 33
        ||| ||| || : ||: : ::
Db      220 LFFALRVLLSRSLRSSTVLQN 241
```

RESULT 6

```
US-10-953-349-29519
; Sequence 29519, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29519
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-29519
```

```
Query Match          29.6%; Score 47; DB 6; Length 367;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      13 FFVFRVLRSSRRVLRSAEI 30
        :|:|:| : | |||
Db      135 YFLFQLLRGLKYLHSAEI 152
```

RESULT 7

US-11-056-355B-69209

; Sequence 69209, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brover, Vyacheslav
 ; APPLICANT: Alexandrov, Nickolai
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; TITLE OF INVENTION: Polypeptides Encoded Thereby
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT APPLICATION NUMBER: US/11/056,355B
 ; CURRENT FILING DATE: 2005-02-14
 ; PRIOR APPLICATION NUMBER: 60/544,190
 ; PRIOR FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO 69209
 ; LENGTH: 367
 ; TYPE: prt
 ; ORGANISM: Triticum aestivum
 ; FEATURE:
 ; NAME/KEY: peptide
 ; LOCATION: (1)..(367)
 ; OTHER INFORMATION: Ceres Seq. ID no. 13656504
 US-11-056-355B-69209

Query Match 29.6%; Score 47; DB 7; Length 367;
 Best Local Similarity 50.0%; Pred. No. 23;
 Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 13 FFVFRVLRSSRVLRSAEI 30
 :|:|:| : | |||
 Db 135 YFLFQLLRGLKYLHSAEI 152

RESULT 8

US-10-953-349-29518

; Sequence 29518, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nickolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; TITLE OF INVENTION: ENCODED THERBY
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 29518
 ; LENGTH: 369
 ; TYPE: PRT
 ; ORGANISM: Triticum aestivum
 US-10-953-349-29518

Query Match 29.6%; Score 47; DB 6; Length 369;
 Best Local Similarity 50.0%; Pred. No. 23;
 Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 13 FFVFRVLRSSRVLRSAEI 30
 :|:|:| : | |||
 Db 137 YFLFQLLRGLKYLHSAEI 154

RESULT 9

US-11-056-355B-69208

; Sequence 69208, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brover, Vyacheslav
 ; APPLICANT: Alexandrov, Nickolai
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; TITLE OF INVENTION: Polypeptides Encoded Thereby
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT APPLICATION NUMBER: US/11/056,355B
 ; CURRENT FILING DATE: 2005-02-14

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OM protein - protein search, using sw model

Run on: August 17, 2006, 15:26:47 ; Search time 39 Seconds
(without alignments)
81.414 Million cell updates/sec

Title: US-10-519-539-127
Perfect score: 159
Sequence: 1 GSRCIRRRISILFFVFRVLRSSRVLRSAEIYES 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	32.1	454	2	T34311	hypothetical prote
2	50	31.4	401	2	AE3186	hypothetical prote
3	49.5	31.1	982	2	E88465	protein B0244.6 [i
4	49	30.8	425	2	AH0122	probable drug effl
5	48.5	30.5	1852	2	A37860	calcium channel pr
6	48	30.2	332	2	H87579	ABC transporter, A
7	48	30.2	341	2	E89856	hypothetical prote
8	47	29.6	252	2	B83706	hypothetical prote
9	47	29.6	487	2	H97304	uncharacterized co
10	46.5	29.2	197	2	A44363	voltage-gated dihy
11	46.5	29.2	575	2	T30021	hypothetical prote
12	46.5	29.2	700	1	S01013	kexin (EC 3.4.21.6
13	46.5	29.2	814	1	KXBY	kexin (EC 3.4.21.6
14	46	28.9	222	2	G87523	cell division ATP-
15	46	28.9	261	2	B95054	sortase, probable
16	46	28.9	510	2	F96987	2,3-bisphosphoglyc
17	46	28.9	562	2	B70081	hypothetical prote
18	45.5	28.6	61	2	C69260	hypothetical prote
19	45.5	28.6	264	2	E75161	shikimate 5-dehydr
20	45.5	28.6	283	2	C23660	calcium channel pr

21	45.5	28.6	294	2	A23660	calcium channel pr
22	45.5	28.6	294	2	B23660	calcium channel pr
23	45.5	28.6	387	2	D84700	hypothetical prote
24	45.5	28.6	1331	2	S05011	calcium channel al
25	45.5	28.6	1610	2	A46227	voltage-dependent
26	45.5	28.6	1646	2	JH0422	voltage-dependent
27	45.5	28.6	2139	2	A44467	voltage-dependent
28	45.5	28.6	2143	2	JH0427	voltage-dependent
29	45.5	28.6	2161	2	JH0564	calcium channel al
30	45.5	28.6	2166	2	S11339	calcium channel pr
31	45.5	28.6	2171	2	S05054	calcium channel al
32	45.5	28.6	2181	2	A38198	calcium channel al
33	45.5	28.6	2203	2	T42742	voltage-dependent
34	45.5	28.6	2220	2	A45290	calcium channel pr
35	45	28.3	171	2	B83184	hypothetical prote
36	45	28.3	268	2	A70417	hypothetical prote
37	45	28.3	411	2	D64884	conserved hypothet
38	45	28.3	780	2	D90753	hypothetical prote
39	45	28.3	780	2	B85617	hypothetical prote
40	45	28.3	791	2	G81109	ribonuclease II fa
41	45	28.3	1126	2	A96032	probable two-compo
42	44.5	28.0	343	2	A35639	G protein-coupled
43	44.5	28.0	347	2	S12955	calcium channel pr
44	44.5	28.0	369	2	AH3551	ABC transporter AT
45	44.5	28.0	373	2	A41918	transforming growt

ALIGNMENTS

RESULT 1

T34311

hypothetical protein F55C12.1 - *Caenorhabditis elegans*C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: T34311

R;Latreille, P.

submitted to the EMBL Data Library, November 1995

A;Description: The sequence of *C. elegans* cosmid F55C12.

A;Reference number: Z21503

A;Accession: T34311

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-454

A;Cross-references: UNIPROT:Q20813; UNIPARC:UPI0000079749; EMBL:U41107; PIDN:AAC71161.1; GSPDB:GN00020; CES

A;Experimental source: strain Bristol N2; clone F55C12

C;Genetics:

A;Gene: CESP:F55C12.1

A;Map position: 2

A;Introns: 52/3; 274/2; 334/1

Query Match 32.1%; Score 51; DB 2; Length 454;

Best Local Similarity 52.4%; Pred. No. 7.5;

Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 5 IRRRISILFFVFRVLRSRRL 25

:|||||:| | :: ||||:

Db 341 VRRRISVLANVVVIIDSRRL 361

RESULT 2

AE3186

hypothetical protein proV [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont) plasmid ATC;Species: *Agrobacterium tumefaciens*

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C;Accession: AE3186

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Kitajima, J.P.;

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, B.; Liao, L.; Kim,

A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AE3186

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-401

A;Cross-references: UNIPROT:Q8UKA5; UNIPARC:UPI00000D153B; GB:AE008687; PIDN:AAL45907.1; PID:g17743653; GSF

A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: proV
 A;Genome: plasmid

Query Match 31.4%; Score 50; DB 2; Length 401;
 Best Local Similarity 41.7%; Pred. No. 9.5;
 Matches 10; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 6 RRRISILFFVFRVLSRRVLSAE 29
 |||:|::| | :| :: | : :||
 Db 105 RRRVSMVFQHFALLPNKTVIENAE 128

RESULT 3

E88465

protein B0244.6 [imported] - *Caenorhabditis elegans*C;Species: *Caenorhabditis elegans*

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: E88465

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology.

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/ for a list of
 A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 285, 1493,

A;Accession: E88465

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-982

A;Cross-references: UNIPROT:Q09965; UNIPARC:UPI000013C084; GB:chr_III; PIDN:AAA68379.1; PID:g861359; GSPDB:

C;Genetics:

A;Gene: B0244.6

A;Map position: 3

Query Match 31.1%; Score 49.5; DB 2; Length 982;
 Best Local Similarity 42.4%; Pred. No. 25;
 Matches 14; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

Qy 2 SRCIRRRISILFFVF-RVLSRRVLSAEIYES 33
 | |: | :||| | :|| | |: : |
 Db 435 SVCLVFTIAILFFVFISLVRSSRKLKRSNTLSS 467

RESULT 4

AH0122

probable drug efflux protein YPO1000 [imported] - *Yersinia pestis* (strain CO92)C;Species: *Yersinia pestis*

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C;Accession: AH0122

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; Sebahia, M.; Jan
 Nature 413, 523-527, 2001A;Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AH0122

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-425

A;Cross-references: UNIPROT:Q8ZHA5; UNIPARC:UPI00000DCA78; GB:AL590842; PIDN:CAC89843.1; PID:g15979068; GSF

C;Genetics:

A;Gene: YPO1000

Query Match 30.8%; Score 49; DB 2; Length 425;
 Best Local Similarity 55.0%; Pred. No. 14;
 Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 8 RISILFFVFRVLSRRVLS 27
 | : :|:| | ||| :|||
 Db 8 RSTPIFYVPRTLRSRLILRS 27

RESULT 5

A37860

calcium channel protein alpha-1 chain, skeletal muscle - common carp

C;Species: *Cyprinus carpio* (common carp)

C;Date: 31-May-1991 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C;Accession: A37860
R;Grabner, M.; Friedrich, K.; Knaus, H.G.; Striessnig, J.; Scheffauer, F.; Staudinger, R.; Koch, W.J.; Schw
Proc. Natl. Acad. Sci. U.S.A. 88, 727-731, 1991
A;Title: Calcium channels from *Cyprinus carpio* skeletal muscle.
A;Reference number: A37860; MUID:91126068; PMID:1846962
A;Accession: A37860
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1852
A;Cross-references: UNIPROT:P22316; UNIPARC:UPI0000127281; GB:M62554; GB:M37203; NID:g213049; PIDN:AAA49205
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: glycoprotein; phosphoprotein; skeletal muscle; transmembrane protein
F;74-90/Domain: transmembrane #status predicted
F;108-131/Domain: transmembrane #status predicted
F;140-158/Domain: transmembrane #status predicted
F;212-234/Domain: transmembrane #status predicted
F;328-350/Domain: transmembrane #status predicted
F;448-466/Domain: transmembrane #status predicted
F;484-501/Domain: transmembrane #status predicted
F;514-530/Domain: transmembrane #status predicted
F;577-596/Domain: transmembrane #status predicted
F;650-676/Domain: transmembrane #status predicted
F;817-834/Domain: transmembrane #status predicted
F;853-870/Domain: transmembrane #status predicted
F;884-901/Domain: transmembrane #status predicted
F;947-966/Domain: transmembrane #status predicted
F;1057-1084/Domain: transmembrane #status predicted
F;1135-1153/Domain: transmembrane #status predicted
F;1169-1188/Domain: transmembrane #status predicted
F;1197-1215/Domain: transmembrane #status predicted
F;1291-1310/Domain: transmembrane #status predicted
F;1377-1402/Domain: transmembrane #status predicted
F;99,102,274,470,813,1157,1269,1485,1703,1713,1745,1760,1848/Binding site: carbohydrate (Asn) (covalent) #s
F;407/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted
F;1471,1523,1738/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted

Query Match 30.5%; Score 48.5; DB 2; Length 1852;
Best Local Similarity 52.2%; Pred. No. 64;
Matches 12; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

Qy 8 RISILFF-VFRVLSRRVLSAE 29
|:| | | :| | | | :| :|
Db 1250 RVSITFFRLFRVLRLIKLLNRSE 1272

RESULT 6

H87579
ABC transporter, ATP-binding protein CC2669 [imported] - *Caulobacter crescentus*
C:Species: *Caulobacter crescentus*
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: H87579
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F.; Alley, M.; Ohta
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: H87579
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-332
A:Cross-references: UNIPROT:Q9A502; UNIPARC:UPI00000C77D9; GB:AE005673; NID:g13424252; PIDN:AAK24636.1; GSF
C:Genetics:
A:Gene: CC2669

Query Match 30.2%; Score 48; DB 2; Length 332;
Best Local Similarity 33.3%; Pred. No. 16;
Matches 9; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 1 GSRCIRRRISILFFVFRVLRSSRRVLRS 27
| | :||: ::| | : | : | ::
Db 74 GLRALRRRVGMIFOHENLLSGKTVAON 100

RESULT 7

E89856
hypothetical protein SA0769 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E89856
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Aoki, K.; N
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E89856
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-341
A;Cross-references: UNIPROT:Q99VG8; UNIPARC:UPI00000CAC48; GB:BA000018; PID:g13700711; PIDN:BAB42008.1; GSF
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA0769
C;Superfamily: probable ABC-type transport protein abc; ATP-binding cassette homology

Query Match 30.2%; Score 48; DB 2; Length 341;
Best Local Similarity 37.0%; Pred. No. 16;
Matches 10; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

```
Qy      1  GSRCIRRRISILFFVFRVLRSRRLRS 27
      | | |:::| | :| || ||::
Db      76 GLRAKROKVNMI FOHFNLLWSRTVLKN 102
```

RESULT 8

B83706
hypothetical protein BH0450 [imported] - *Bacillus halodurans* (strain C-125)
C:Species: *Bacillus halodurans*
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: B83706
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirama, C.; Nakamura, Y.
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and genomic sequence co
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83706
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-252
A;Cross-references: UNIPROT:Q9KFM9; UNIPARC:UPI00000C38A5; GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BA
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0450

Query Match 29.6%; Score 47; DB 2; Length 252;
Best Local Similarity 37.5%; Pred. No. 17;
Matches 9; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 10 SILFFVFRVLRSSRVLRSAEIIYES 33
|:|::| :::| || : |:|
Db 162 SLLFYLFMLIKSSRVALAISIFLS 185

RESULT 9

H97304
uncharacterized conserved membrane protein CAC3293 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97304
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, H.M.; Dubois, J.;
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutyl
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97304
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-487
A;Cross-references: UNIPROT:Q97E23; UNIPARC:UPI00000CA7A7; GB:AE001437; PIDN:AAK81227.1; PID:g15026371; GSF
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC3293

Query Match 29.6%; Score 47; DB 2; Length 487;
Best Local Similarity 26.1%; Pred. No. 32;
Matches 6; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

SCORE Search Results Details for Application 10519539 and Search Result us-10-519-539- 127.rup.

[Score Home](#) [Retrieve Application](#) [SCORE System](#) [SCORE](#) [Comments /](#)
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OM protein - protein search, using sw model

Run on: August 17, 2006, 15:23:11 ; Search time 299 Seconds
(without alignments)
102.092 Million cell updates/sec

Title: US-10-519-539-127
Perfect score: 159
Sequence: 1 GSRCIRRRISILFFVFRVLRSSRVLRSAEYES 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	34.6	335	2	Q3BNZ3_XANC5	Q3bnz3 xanthomonas
2	55	34.6	335	2	Q2P7S3_XANOR	Q2p7s3 xanthomonas
3	55	34.6	335	2	Q8PGE8_XANAC	Q8pge8 xanthomonas
4	55	34.6	405	2	Q4CKS0_TRYCR	Q4cks0 trypanosoma
5	54	34.0	93	2	Q2LTA8_9DELT	Q2lta8 syntrophus
6	54	34.0	335	2	Q4UQD2_XANC8	Q4uqd2 xanthomonas
7	54	34.0	335	2	Q8P4S7_XANCP	Q8p4s7 xanthomonas
8	54	34.0	1041	2	Q4CNG6_TRYCR	Q4cng6 trypanosoma
9	53	33.3	1753	2	Q4QGC7_LEIMA	Q4qgc7 leishmania
10	52.5	33.0	79	2	Q93FQ5_EHRRU	Q93fq5 ehrlichia r
11	52	32.7	148	2	Q3RM07_RALME	Q3rm07 ralstonia m
12	52	32.7	400	2	Q5H503_XANOR	Q5h503 xanthomonas
13	52	32.7	436	2	Q666F1_YERPS	Q666f1 yersinia ps
14	51.5	32.4	738	2	Q8SVC1_ENCCU	Q8svc1 encephalito
15	51	32.1	49	2	Q8FCF0_ECOL6	Q8fcf0 escherichia

16	51	32.1	176	2	Q5TRV5_ANOGA	Q5trv5 anopheles g
17	51	32.1	341	2	Q2YWP2_STAAB	Q2ywp2 staphylococ
18	51	32.1	341	2	Q5HHK4_STAAC	Q5hkh4 staphylococ
19	51	32.1	341	2	Q6GB18_STAAS	Q6gb18 staphylococ
20	51	32.1	341	2	Q6GIH9_STAAR	Q6gih9 staphylococ
21	51	32.1	341	2	Q8NXH5_STAAS	Q8nxh5 staphylococ
22	51	32.1	395	2	Q3F5D0_9BURK	Q3f5d0 burkholderi
23	51	32.1	416	2	Q8IG14_CAEEL	Q8ig14 caenorhabdi
24	51	32.1	454	2	Q20813_CAEEL	Q20813 caenorhabdi
25	51	32.1	468	2	Q8IG15_CAEEL	Q8ig15 caenorhabdi
26	51	32.1	471	2	Q95ZS6_CAEEL	Q95zs6 caenorhabdi
27	51	32.1	614	1	ALG10_ASPFU	Q4x162 aspergillus
28	51	32.1	684	2	Q7VIS2_HELHP	Q7vis2 helicobacte
29	51	32.1	1071	2	Q34YD5_9GAMM	Q34yd5 alkalilimni
30	50.5	31.8	944	2	Q8IK70_PLAF7	Q8ik70 plasmodium
31	50	31.4	344	2	Q4BFY9_BURVI	Q4bfy9 burkholderi
32	50	31.4	401	2	Q8UKA5_AGR5	Q8uka5 agrobacteri
33	50	31.4	475	2	Q972D9_SULTO	Q972d9 sulfolobus
34	50	31.4	610	2	Q9FND8_ARATH	Q9fnd8 arabidopsis
35	50	31.4	1030	2	Q8ALV7_BACTN	Q8alv7 bacteroides
36	50	31.4	1228	2	Q4CUC0_TRYCR	Q4cuc0 trypanosoma
37	50	31.4	1230	2	Q4DVL1_TRYCR	Q4dvl1 trypanosoma
38	49.5	31.1	982	1	YS96_CAEEL	Q09965 caenorhabdi
39	49	30.8	322	2	Q95XD5_CAEEL	Q95xd5 caenorhabdi
40	49	30.8	425	2	Q74QQ1_YERPE	Q74qq1 yersinia pe
41	49	30.8	425	2	Q8ZHA5_YERPE	Q8zha5 yersinia pe
42	49	30.8	463	2	Q7RIE9_PLAYO	Q7rie9 plasmodium
43	49	30.8	472	2	Q9J2K6_9GAMA	Q9j2k6 rhesus monk
44	49	30.8	480	2	Q9WRR4_9GAMA	Q9wrr4 macaca mula
45	49	30.8	497	2	Q2S4J7_9SPHI	Q2s4j7 salinibacte

ALIGNMENTS

RESULT 1

Q3BNZ3_XANC5

ID Q3BNZ3_XANC5 PRELIMINARY; PRT; 335 AA.
AC Q3BNZ3;
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 22-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE D-methionine ABC transporter ATP-binding protein.
GN Name=metN; OrderedLocusNames=XCV3789;
OS Xanthomonas campestris pv. vesicatoria (strain 85-10).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=316273;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16237009; DOI=10.1128/JB.187.21.7254-7266.2005;
RA Thieme F., Koebe R., Bekel T., Berger C., Boch J., Buettner D.,
RA Caldana C., Gaigalat L., Goesmann A., Kay S., Kirchner O., Lanz C.,
RA Linke B., McHardy A.C., Meyer F., Mittenhuber G., Nies D.H.,
RA Niesbach-Kloesgen U., Patschkowski T., Rueckert C., Rupp O.,
RA Schneiker S., Schuster S.C., Vorhoeelter F.J., Weber E., Puehler A.,
RA Bonas U., Bartels D., Kaiser O.;
RT "Insights into genome plasticity and pathogenicity of the plant
RT pathogenic Bacterium Xanthomonas campestris pv. vesicatoria revealed
RT by the complete genome sequence."
RL J. Bacteriol. 187:7254-7266(2005).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
CC -----
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CC -----
DR EMBL; AM039952; CAJ25520.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.
SQ SEQUENCE 335 AA; 36380 MW; 906AFEF95A138F62 CRC64;

Query Match 34.6%; Score 55; DB 2; Length 335;
Best Local Similarity 50.0%; Pred. No. 14;

Matches 12; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GSRCIRRRISILFFVFRVLRSSRV 24
 | | :| | | :| | :| | |
 Db 76 GLRALRRRIGMIFQHFNLLSSRTV 99

RESULT 2

Q2P7S3_XANOR

ID Q2P7S3_XANOR PRELIMINARY; PRT; 335 AA.
 AC Q2P7S3;
 DT 07-FEB-2006, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, sequence version 1.
 DT 07-FEB-2006, entry version 1.
 DE ABC transporter ATP-binding protein.
 GN Name=XOO0649;
 OS Xanthomonas oryzae pv. oryzae MAFF 311018.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=342109;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MAFF 311018;
 RA Ochiai H., Inoue Y., Takeya M., Sasaki A., Kaku H.;
 RT "Genome sequence of Xanthomonas oryzae pv. oryzae suggests
 RT contribution of large numbers of effector genes and insertion
 RT sequences to its race diversity.";
 RL Jpn. Agric. Res. Q. 39:275-287(2005).
 CC -----
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 CC -----
 DR EMBL; AP008229; BAE67404.1; -; Genomic_DNA.
 KW ATP-binding.
 SQ SEQUENCE 335 AA; 36346 MW; E016F04D775039E9 CRC64;

Query Match 34.6%; Score 55; DB 2; Length 335;
 Best Local Similarity 50.0%; Pred. No. 14;
 Matches 12; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GSRCIRRRISILFFVFRVLRSSRV 24
 | | :| | | :| | :| | |
 Db 76 GLRALRRRIGMIFQHFNLLSSRTV 99

RESULT 3

Q8PGE8_XANAC

ID Q8PGE8_XANAC PRELIMINARY; PRT; 335 AA.
 AC Q8PGE8;
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2002, sequence version 1.
 DT 07-FEB-2006, entry version 21.
 DE ABC transporter ATP-binding protein.
 GN Name=abc;
 OS Xanthomonas axonopodis pv. citri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=92829;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=306 / ATCC 13902 / XV 101;
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,
 RA Almeida N.F. Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,
 RA Camargo L.E.A., Camarotte G., Cannavan F., Cardozo J., Chambergo F.,
 RA Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,
 RA El-Dorriy H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,
 RA Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities.";
 RL Nature 417:459-463(2002).
 CC -!- SIMILARITY: Belongs to the ABC transporter family.
 CC -----
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 CC -----
 DR EMBL; AE012017; AAM38512.1; -; Genomic_DNA.
 DR HSSP; P02915; 1B0U.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0016887; F:ATPase activity; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transp_like.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.
 SQ SEQUENCE 335 AA; 36516 MW; 9061353B5DE4ABC3 CRC64;

Query Match 34.6%; Score 55; DB 2; Length 335;
 Best Local Similarity 50.0%; Pred. No. 14;
 Matches 12; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GSRCIRRRISILFFVFRVLRSSRV 24
 | | :| | | :| | :| | |
 Db 76 GLRALRRRIGMIFQHFNLLSSRTV 99

RESULT 4

Q4CKS0_TRYCR

ID Q4CKS0_TRYCR PRELIMINARY; PRT; 405 AA.
 AC Q4CKS0;
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 07-FEB-2006, entry version 2.
 DE Hypothetical protein (Fragment).
 GN ORFNames=Tc00.1047053452039.9;
 OS Trypanosoma cruzi.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
 OC Schizotrypanum.
 OX NCBI_TaxID=5693;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CL Brener;
 RA El-Sayed N.M.A., Myler P.J., Bartholomeu D.C., Nilsson D.,
 RA Aggarwal G., Tran A.-N., Ghedin E., Worthey E.A., Delcher A.L.,
 RA Blandin G., Westenberger S.J., Caler E., Cerqueira G.C., Branche C.,
 RA Haas B., Anapuma A., Arner E., Aslund L., Attipoe P., Bontempi E.,
 RA Bringaud F., Burton P., Cadag E., Campbell D.A., Carrington M.,
 RA Crabtree J., Darban H., da Silveira J.F., de Jong P., Edwards K.,
 RA Englund P.T., Fazelina G., Feldblyum T., Ferella M., Frasch A.C.,
 RA Gull K., Horn D., Hou L., Huang Y., Kindlund E., Klingbeil M.,
 RA Kluge S., Koo H., Lacerda D., Levin M.J., Lorenzi H., Louie T.,
 RA Machado C.R., McCulloch R., McKenna A., Mizuno Y., Mottram J.C.,
 RA Nelson S., Ochaya S., Osoegawa K., Pai G., Parsons M., Pentony M.,
 RA Pettersson U., Pop M., Ramirez J.L., Rinta J., Robertson L.,
 RA Salzberg S.L., Sanchez D.O., Seyler A., Sharma R., Shetty J.,
 RA Simpson A.J., Sisk E., Tammi M.T., Tarleton R., Teixeira S.,
 RA Van Aken S., Vogt C., Ward P.N., Wickstead B., Wortman J., White O.,
 RA Fraser C.M., Stuart K.D., Andersson B.;
 RT "The Genome Sequence of Trypanosoma cruzi, Etiologic Agent of Chagas'
 RT Disease.";
 RL Science 0:0-0(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CL Brener;
 RA El-Sayed N.M.A., Myler P.J., Blandin G., Berriman M., Crabtree J.,
 RA Aggarwal G., Caler E., Renauld H., Worthey E.A., Hertz-Fowler C.,
 RA Ghedin E., Peacock C., Bartholomeu D.C., Haas B.J., Tran A.-N.,
 RA Wortman J.R., Alsmark U.C.M., Angiuoli S., Anupama A., Badger J.,

RA Bringaud F., Cadag E., Carlton J.M., Cerqueira G.C., Creasy T.,
 RA Delcher A.L., Djikeng A., Embley T.M., Hauser C., Ivens A.C.,
 RA Kummerfeld S.K., Pereira-Leal J.B., Nilsson D., Peterson J.,
 RA Salzberg S.L., Shallom J., Silva J.C., Sundaram J., Westenberger S.,
 RA White O., Melville S.E., Donelson J.E., Andersson B., Stuart K.D.,
 RA Hall N.;
 RT "Comparative Genomics of Trypanosomatid Parasitic Protozoa.";
 RL Science 0:0-0(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CL Brener;
 RA El-Sayed N., Bartholomeu D., Haas B.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AAHK01006472; EAN80872.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON_TER 1 1
 SQ SEQUENCE 405 AA; 45340 MW; BD528F8432BD8BC6 CRC64;

Query Match 34.6%; Score 55; DB 2; Length 405;
 Best Local Similarity 57.1%; Pred. No. 17;
 Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GSRCIRRRISILFFVFRVLR 21
 I: |||:|:| |||||
 Db 212 GTLLSARRITIIFFVFRVLRNS 232

RESULT 5

Q2LTA8_9DELT
 ID Q2LTA8_9DELT PRELIMINARY; PRT; 93 AA.
 AC Q2LTA8;
 DT 21-FEB-2006, integrated into UniProtKB/TrEMBL.
 DT 21-FEB-2006, sequence version 1.
 DT 21-FEB-2006, entry version 1.
 DE Hypothetical membrane protein.
 GN ORFNames=SYN_02164;
 OS Syntrophus aciditrophicus SB.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Syntrophobacterales;
 OC Syntrophaceae; Syntrophus.
 OX NCBI_TaxID=56780;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gunsalus R., Rohlin L., Kim U., Krupp R., Bhattacharyya A.,
 RA Campbell J., McIerney M., Moutakki H., Rio-Hernandez L.;
 RT "The genome of the syntrophic bacterium Syntrophus aciditrophicus:
 RT Life dependent on negative change in electrical potential.";
 RL Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; CP000252; ABC77315.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 93 AA; 10724 MW; 45BC124B9559D09A CRC64;

Query Match 34.0%; Score 54; DB 2; Length 93;
 Best Local Similarity 52.4%; Pred. No. 5.5;
 Matches 11; Conservative 6; Mismatches 2; Indels 2; Gaps 1;

Qy 9 ISILFFVFRVLRSRVLRSAE 29
 : :|: :||| :|:||||
 Db 11 VIVLYLIFRVLR--KRILRSAR 29

RESULT 6

Q4UQD2_XANC8
 ID Q4UQD2_XANC8 PRELIMINARY; PRT; 335 AA.
 AC Q4UQD2;
 DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.

SCORE Search Results Details for Application 10519539 and Search Result us-10-519-539-127.rapbm.

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OM protein - protein search, using sw model

Run on: August 17, 2006, 15:32:26 ; Search time 184 Seconds
(without alignments)
83.077 Million cell updates/sec

Title: US-10-519-539-127
Perfect score: 159
Sequence: 1 GSR CIRRRISILFFVFRVLRSSRRVLRSAEIIYES 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	159	100.0	33	5	US-10-519-539-79	Sequence 79, Appl
2	159	100.0	33	5	US-10-519-539-127	Sequence 127, App
3	75.5	47.5	32	5	US-10-519-539-81	Sequence 81, Appl
4	75.5	47.5	32	5	US-10-519-539-129	Sequence 129, App
5	73.5	46.2	32	5	US-10-519-539-105	Sequence 105, App
6	73.5	46.2	34	5	US-10-519-539-57	Sequence 57, Appl
7	69	43.4	35	5	US-10-519-539-63	Sequence 63, Appl
8	67.5	42.5	33	5	US-10-519-539-75	Sequence 75, Appl
9	67.5	42.5	33	5	US-10-519-539-123	Sequence 123, App
10	65	40.9	33	5	US-10-519-539-104	Sequence 104, App
11	65	40.9	35	5	US-10-519-539-56	Sequence 56, Appl

12	63	39.6	33	5	US-10-519-539-59	Sequence 59, Appl
13	63	39.6	33	5	US-10-519-539-107	Sequence 107, App
14	62.5	39.3	32	5	US-10-519-539-66	Sequence 66, Appl
15	62.5	39.3	32	5	US-10-519-539-114	Sequence 114, App
16	62.5	39.3	32	5	US-10-519-539-122	Sequence 122, App
17	62.5	39.3	34	5	US-10-519-539-74	Sequence 74, Appl
18	61	38.4	32	5	US-10-519-539-44	Sequence 44, Appl
19	61	38.4	32	5	US-10-519-539-92	Sequence 92, Appl
20	59	37.1	33	5	US-10-519-539-98	Sequence 98, Appl
21	59	37.1	35	5	US-10-519-539-50	Sequence 50, Appl
22	58.5	36.8	33	5	US-10-519-539-115	Sequence 115, App
23	58.5	36.8	35	5	US-10-519-539-67	Sequence 67, Appl
24	56.5	35.5	32	5	US-10-519-539-71	Sequence 71, Appl
25	56.5	35.5	32	5	US-10-519-539-119	Sequence 119, App
26	56	35.2	33	5	US-10-519-539-120	Sequence 120, App
27	56	35.2	35	5	US-10-519-539-72	Sequence 72, Appl
28	55	34.6	32	5	US-10-519-539-73	Sequence 73, Appl
29	55	34.6	32	5	US-10-519-539-121	Sequence 121, App
30	55	34.6	370	4	US-10-767-701-45385	Sequence 45385, A
31	53.5	33.6	32	5	US-10-519-539-60	Sequence 60, Appl
32	53.5	33.6	32	5	US-10-519-539-108	Sequence 108, App
33	53	33.3	281	4	US-10-424-599-148726	Sequence 148726,
34	52.5	33.0	35	5	US-10-519-539-86	Sequence 86, Appl
35	51	32.1	32	5	US-10-519-539-64	Sequence 64, Appl
36	51	32.1	32	5	US-10-519-539-84	Sequence 84, Appl
37	51	32.1	32	5	US-10-519-539-112	Sequence 112, App
38	51	32.1	32	5	US-10-519-539-132	Sequence 132, App
39	51	32.1	33	5	US-10-519-539-77	Sequence 77, Appl
40	51	32.1	33	5	US-10-519-539-125	Sequence 125, App
41	51	32.1	748	4	US-10-425-114-69372	Sequence 69372, A
42	51	32.1	849	5	US-10-450-763-46706	Sequence 46706, A
43	50.5	31.8	33	5	US-10-519-539-100	Sequence 100, App
44	50.5	31.8	35	5	US-10-519-539-52	Sequence 52, Appl
45	50	31.4	79	4	US-10-424-599-219137	Sequence 219137,

ALIGNMENTS

RESULT 1

US-10-519-539-79

; Sequence 79, Application US/10519539

; Publication No. US20050203288A1

; GENERAL INFORMATION:

; APPLICANT: Deutsches Krebsforschungszentrum

; TITLE OF INVENTION: Peptides for inducing apoptosis in tumor cells

; FILE REFERENCE: DK62021PC

; CURRENT APPLICATION NUMBER: US/10/519,539

; CURRENT FILING DATE: 2004-12-28

; NUMBER OF SEQ ID NOS: 132

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 79

; LENGTH: 33

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: randomized peptide that bind to particular IAPs

US-10-519-539-79

Query Match 100.0%; Score 159; DB 5; Length 33;

Best Local Similarity 100.0%; Pred. No. 2.3e-16;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 GSRCIRRRISILFFVFRVLRSSRRVLRSAEIIYES 33
          |||
Db      1 GSRCIRRRISILFFVFRVLRSSRRVLRSAEIIYES 33

```

RESULT 2

US-10-519-539-127

; Sequence 127, Application US/10519539

; Publication No. US20050203288A1

; GENERAL INFORMATION:

; APPLICANT: Deutsches Krebsforschungszentrum

; TITLE OF INVENTION: Peptides for inducing apoptosis in tumor cells

; FILE REFERENCE: DK62021PC

```
; CURRENT APPLICATION NUMBER: US/10/519,539
; CURRENT FILING DATE: 2004-12-28
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: randomized peptide that bind to particular IAPs
US-10-519-539-127
```

```
Query Match          100.0%; Score 159; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GSR CIRRRISILFFVFRVLR SRRVLRSAEIYES 33
         |||||
Db      1 GSR CIRRRISILFFVFRVLR SRRVLRSAEIYES 33
```

RESULT 3

US-10-519-539-81

```
; Sequence 81, Application US/10519539
; Publication No. US20050203288A1
; GENERAL INFORMATION:
; APPLICANT: Deutsches Krebsforschungszentrum
; TITLE OF INVENTION: Peptides for inducing apoptosis in tumor cells
; FILE REFERENCE: DK62021PC
; CURRENT APPLICATION NUMBER: US/10/519,539
; CURRENT FILING DATE: 2004-12-28
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: randomized peptide that bind to particular IAPs
US-10-519-539-81
```

```
Query Match          47.5%; Score 75.5; DB 5; Length 32;
Best Local Similarity 63.6%; Pred. No. 0.00068;
Matches 21; Conservative 1; Mismatches 10; Indels 1; Gaps 1;
```

```
Qy      1 GSR CIRRRISILFFVFRVLR SRRVLRSAEIYES 33
         | : || || | ||| |||||
Db      1 GPSSLLRCLILGMVLGVLR-RRVLRSAEIYES 32
```

RESULT 4

US-10-519-539-129

```
; Sequence 129, Application US/10519539
; Publication No. US20050203288A1
; GENERAL INFORMATION:
; APPLICANT: Deutsches Krebsforschungszentrum
; TITLE OF INVENTION: Peptides for inducing apoptosis in tumor cells
; FILE REFERENCE: DK62021PC
; CURRENT APPLICATION NUMBER: US/10/519,539
; CURRENT FILING DATE: 2004-12-28
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: randomized peptide that bind to particular IAPs
US-10-519-539-129
```

```
Query Match          47.5%; Score 75.5; DB 5; Length 32;
Best Local Similarity 63.6%; Pred. No. 0.00068;
Matches 21; Conservative 1; Mismatches 10; Indels 1; Gaps 1;
```

```
Qy      1 GSR CIRRRISILFFVFRVLR SRRVLRSAEIYES 33
         | : || || | ||| |||||
```

Db 1 GPSSLLRRCLILGMVLGVLR-RRVLRSAEIIYES 32

RESULT 5

US-10-519-539-105

; Sequence 105, Application US/10519539

; Publication No. US20050203288A1

; GENERAL INFORMATION:

; APPLICANT: Deutsches Krebsforschungszentrum

; TITLE OF INVENTION: Peptides for inducing apoptosis in tumor cells

; FILE REFERENCE: DK62021PC

; CURRENT APPLICATION NUMBER: US/10/519,539

; CURRENT FILING DATE: 2004-12-28

; NUMBER OF SEQ ID NOS: 132

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 105

; LENGTH: 32

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: randomized peptide that bind to particular IAPs

US-10-519-539-105

Query Match 46.2%; Score 73.5; DB 5; Length 32;

Best Local Similarity 60.0%; Pred. No. 0.0014;

Matches 18; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

Qy 4 CIRRRISILFFVFRVLRSSRVLRSAEIIYES 33

Db 4 CSLCRMVLMFVLRGIR-LRVLRSAEIIYES 32

RESULT 6

US-10-519-539-57

; Sequence 57, Application US/10519539

; Publication No. US20050203288A1

; GENERAL INFORMATION:

; APPLICANT: Deutsches Krebsforschungszentrum

; TITLE OF INVENTION: Peptides for inducing apoptosis in tumor cells

; FILE REFERENCE: DK62021PC

; CURRENT APPLICATION NUMBER: US/10/519,539

; CURRENT FILING DATE: 2004-12-28

; NUMBER OF SEQ ID NOS: 132

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 57

; LENGTH: 34

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: randomized peptide that bind to particular IAPs

US-10-519-539-57

Query Match 46.2%; Score 73.5; DB 5; Length 34;

Best Local Similarity 60.0%; Pred. No. 0.0014;

Matches 18; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

Qy 4 CIRRRISILFFVFRVLRSSRVLRSAEIIYES 33

Db 6 CSLCRMVLMFVLRGIR-LRVLRSAEIIYES 34

RESULT 7

US-10-519-539-63

; Sequence 63, Application US/10519539

; Publication No. US20050203288A1

; GENERAL INFORMATION:

; APPLICANT: Deutsches Krebsforschungszentrum

; TITLE OF INVENTION: Peptides for inducing apoptosis in tumor cells

; FILE REFERENCE: DK62021PC

; CURRENT APPLICATION NUMBER: US/10/519,539

; CURRENT FILING DATE: 2004-12-28

; NUMBER OF SEQ ID NOS: 132

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 63

; LENGTH: 35

; TYPE: PRT

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: randomized peptide that bind to particular IAPs
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (19)..(19)
; OTHER INFORMATION: undefined amino acid
US-10-519-539-63

```

Query Match 43.4%; Score 69; DB 5; Length 35;
Best Local Similarity 51.3%; Pred. No. 0.007;
Matches 20; Conservative 2; Mismatches 5; Indels 12; Gaps 2;

Qy 1 GSRCIRRRISI-----LFFVFRVLSRRVLSAEIYES 33
|| |:| |:| | ||| |||||

Db 3 GSGCVRIRVGIVRRMLXLRFFV-----LVLSAEIYES 35

RESULT 8

```

US-10-519-539-75
; Sequence 75, Application US/10519539
; Publication No. US20050203288A1
; GENERAL INFORMATION:
; APPLICANT: Deutsches Krebsforschungszentrum
; TITLE OF INVENTION: Peptides for inducing apoptosis in tumor cells
; FILE REFERENCE: DK62021PC
; CURRENT APPLICATION NUMBER: US/10/519,539
; CURRENT FILING DATE: 2004-12-28
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: randomized peptide that bind to particular IAPs
US-10-519-539-75

```

Query Match 42.5%; Score 67.5; DB 5; Length 33;
Best Local Similarity 58.1%; Pred. No. 0.011;
Matches 18; Conservative 3; Mismatches 7; Indels 3; Gaps 1;

```

Qy      3 RCIRRRISILFFVFRVLSRRVLSRAEIYES 33
      | | | | : | : | : | | | | | | |
Db      6 RVIRLRIVVLRICIFLLF---RVLRS AEIYES 33

```

RESULT 9

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US-10-519-539-123
; Sequence 123, Application US/10519539
; Publication No. US20050203288A1
; GENERAL INFORMATION:
; APPLICANT: Deutsches Krebsforschungszentrum
; TITLE OF INVENTION: Peptides for inducing apoptosis in tumor cells
; FILE REFERENCE: DK62021PC
; CURRENT APPLICATION NUMBER: US/10/519,539
; CURRENT FILING DATE: 2004-12-28
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: randomized peptide that bind to particular IAPs
US-10-519-539-123
```

Query Match 42.5%; Score 67.5; DB 5; Length 33;
Best Local Similarity 58.1%; Pred. No. 0.011;
Matches 18; Conservative 3; Mismatches 7; Indels 3; Gaps 1;

```

Qy      3 RCIRRRISILFFVFRVLSRRVLSRAEIYES 33
      | | | | : | : | : | | | | | | | |
Db      6 RVIRLRIVVLRCIFLLF---RVLRS AEIYES 33

```

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OM protein - protein search, using sw model

Run on: August 17, 2006, 15:22:26 ; Search time 204 Seconds
(without alignments)
73.961 Million cell updates/sec

Title: US-10-519-539-127
Perfect score: 159
Sequence: 1 GSRCIRRRISILFFVFRVLRSSRVLRSAEIYES 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	159	100.0	33	8	ADH39961	Adh39961 Inhibitor
2	75.5	47.5	32	8	ADH39963	Adh39963 Inhibitor
3	73.5	46.2	34	8	ADH39939	Adh39939 Inhibitor
4	69	43.4	35	8	ADH39945	Adh39945 Inhibitor
5	67.5	42.5	33	8	ADH39957	Adh39957 Inhibitor
6	65	40.9	35	8	ADH39938	Adh39938 Inhibitor
7	63	39.6	33	8	ADH39941	Adh39941 Inhibitor

8	62.5	39.3	32	8	ADH39948	Adh39948	Inhibitor
9	62.5	39.3	34	8	ADH39956	Adh39956	Inhibitor
10	61	38.4	32	8	ADH39926	Adh39926	Inhibitor
11	59	37.1	35	8	ADH39932	Adh39932	Inhibitor
12	58.5	36.8	35	8	ADH39949	Adh39949	Inhibitor
13	56.5	35.5	32	8	ADH39953	Adh39953	Inhibitor
14	56	35.2	35	8	ADH39954	Adh39954	Inhibitor
15	55	34.6	32	8	ADH39955	Adh39955	Inhibitor
16	54	34.0	248	9	ABM95918	Abm95918	M. xanthu
17	53.5	33.6	32	8	ADH39942	Adh39942	Inhibitor
18	52.5	33.0	35	8	ADH39968	Adh39968	Inhibitor
19	51	32.1	32	8	ADH39966	Adh39966	Inhibitor
20	51	32.1	32	8	ADH39946	Adh39946	Inhibitor
21	51	32.1	33	8	ADH39959	Adh39959	Inhibitor
22	51	32.1	341	6	ABM72194	Abm72194	Staphyloc
23	51	32.1	748	8	ADY13557	Ady13557	Plant ful
24	51	32.1	849	4	ABG16347	Abg16347	Novel hum
25	50.5	31.8	35	8	ADH39934	Adh39934	Inhibitor
26	50	31.4	162	9	ABM96823	Abm96823	M. xanthu
27	50	31.4	181	6	ABU05997	Abu05997	N. lactam
28	49	30.8	28	8	ADH39958	Adh39958	Inhibitor
29	49	30.8	480	3	AAB53157	Aab53157	Macaca mu
30	49	30.8	791	6	ABP79242	Abp79242	N. gonorr
31	49	30.8	792	3	AAY75754	Aay75754	Neisseria
32	48.5	30.5	32	8	ADH39952	Adh39952	Inhibitor
33	48.5	30.5	32	8	ADH39925	Adh39925	Inhibitor
34	48	30.2	141	5	AAU81326	Aau81326	Novel hum
35	48	30.2	155	8	ADQ65048	Adq65048	Novel hum
36	48	30.2	297	5	AAU81360	Aau81360	Novel hum
37	48	30.2	350	7	ADC97351	Adc97351	E. faeciu
38	48	30.2	418	6	ABP80316	Abp80316	N. gonorr
39	48	30.2	430	4	AAG63970	Aag63970	Amino aci
40	48	30.2	430	7	ADJ69452	Adj69452	Human hea
41	48	30.2	430	8	ADI27922	Adi27922	Human TWI
42	48	30.2	430	8	ADQ89140	Adq89140	Human uro
43	48	30.2	430	8	ADR44926	Adr44926	Polypepti
44	48	30.2	430	8	ADS11104	Ads11104	Human the
45	48	30.2	489	5	AAE13288	Aae13288	Human tra

ALIGNMENTS

RESULT 1

ADH39961

ID ADH39961 standard; peptide; 33 AA.

XX

AC ADH39961;

XX

DT 25-MAR-2004 (first entry)

XX

DE Inhibitor of apoptosis protein (IAP) binding peptide SEQ ID NO:79.

XX

KW inhibitors of apoptosis protein; IAP; IAP binding peptide;

KW apoptosis induction; cytostatic; apoptosis; cancer; neuroblastoma;

KW intestine carcinoma; rectum carcinoma; colon carcinoma;

KW familial adenomatous polyposis carcinoma;

KW hereditary non-polyposis colorectal cancer; oesophageal carcinoma;

KW labial carcinoma; larynx carcinoma; hypopharynx carcinoma;

KW tongue carcinoma; salivary gland carcinoma; gastric carcinoma;

KW adenocarcinoma; medullary thyroid carcinoma;

KW papillary thyroid carcinoma; renal carcinoma;

KW kidney parenchyma carcinoma; ovarian carcinoma; cervix carcinoma;

KW uterine corpus carcinoma; endometrium carcinoma; chorion carcinoma;

KW pancreatic carcinoma; prostate carcinoma; testis carcinoma;

KW breast carcinoma; urinary carcinoma; melanoma; brain tumour;

KW glioblastoma; astrocytoma; meningioma; medulloblastoma;

KW peripheral neuroectodermal tumour; Hodgkin lymphoma;

KW non-Hodgkin lymphoma; Burkitt lymphoma; acute lymphatic leukaemia;

KW chronic lymphatic leukaemia; acute myeloid leukaemia;

KW chronic myeloid leukaemia; adult T-cell leukaemia lymphoma;

KW hepatocellular carcinoma; gall bladder carcinoma; bronchial carcinoma;

KW small cell lung carcinoma; non-small cell lung carcinoma;

KW multiple myeloma; basalioma; teratoma; retinoblastoma;

KW chorioidea melanoma; seminoma; rhabdomyosarcoma; craniopharyngeoma;

KW osteosarcoma; chondrosarcoma; myosarcoma; liposarcoma; fibrosarcoma;

KW Ewing sarcoma; plasmocytoma.
 XX
 OS Synthetic.
 XX
 PN EP1378515-A1.
 XX
 PD 07-JAN-2004.
 XX
 PF 01-JUL-2002; 2002EP-00014074.
 XX
 PR 01-JUL-2002; 2002EP-00014074.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 PI Butz K, Crnkovic-Mertens I, Hoppe-Seyler F, Rausch C;
 XX
 DR WPI; 2004-073742/08.
 XX
 PT Novel peptide binding to inhibitors of apoptosis proteins and inducing
 PT apoptosis, useful for treatment of cancer.
 XX
 PS Claim 1; SEQ ID NO 79; 46pp; English.
 XX
 CC The present invention describes a peptide (I) which binds to inhibitors
 CC of apoptosis proteins (IAPs) and induces apoptosis, its fragment or
 CC derivatives. (I) has cytostatic activity, and can be used as an inducer
 CC of apoptosis. (I), optionally in combination with a active compound is
 CC useful for the manufacture of a medicament for the binding of IAPs, which
 CC are useful for treatment of cancer, where the cancer to be treated is
 CC chosen from the group consisting of neuroblastoma, intestine carcinoma,
 CC preferably rectum carcinoma, colon carcinoma, familial adenomatous
 CC polyposis carcinoma and hereditary non-polyposis colorectal cancer,
 CC oesophageal carcinoma, labial carcinoma, larynx carcinoma, hypopharynx
 CC carcinoma, tongue carcinoma, salivary gland carcinoma, gastric carcinoma,
 CC adenocarcinoma, medullary thyroid carcinoma, papillary thyroid
 CC carcinoma, renal carcinoma, kidney parenchyma carcinoma, ovarian
 CC carcinoma, cervix carcinoma, uterine corpus carcinoma, endometrium
 CC carcinoma, chorion carcinoma, pancreatic carcinoma, prostate carcinoma,
 CC testis carcinoma, breast carcinoma, urinary carcinoma, melanoma, brain
 CC tumours preferably glioblastoma, astrocytoma, meningioma, medulloblastoma
 CC and peripheral neuroectodermal tumours, Hodgkin lymphoma, non-Hodgkin
 CC lymphoma, Burkitt lymphoma, acute lymphatic leukaemia (ALL), chronic
 CC lymphatic leukaemia (CLL), acute myeloid leukaemia (AML), chronic myeloid
 CC leukaemia (CML), adult T-cell leukaemia lymphoma, hepatocellular
 CC carcinoma, gall bladder carcinoma, bronchial carcinoma, small cell lung
 CC carcinoma, non-small cell lung carcinoma, multiple myeloma, basaloma,
 CC teratoma, retinoblastoma, choroid melanoma, seminoma, rhabdomyosarcoma,
 CC craniopharyngeoma, osteosarcoma, chondrosarcoma, myosarcoma, liposarcoma,
 CC fibrosarcoma, Ewing sarcoma and plasmocytoma. The present sequence
 CC represents a randomised peptide that binds to IAPs, which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 33 AA;

Query Match 100.0%; Score 159; DB 8; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.4e-17;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSR CIRRRISILFFVFRVLR SRRLRS AEIYES 33
 |||||
 Db 1 GSR CIRRRISILFFVFRVLR SRRLRS AEIYES 33

RESULT 2

ADH39963

ID ADH39963 standard; peptide; 32 AA.

XX

AC ADH39963;

XX

DT 25-MAR-2004 (first entry)

XX

DE Inhibitor of apoptosis protein (IAP) binding peptide SEQ ID NO:81.

XX

KW inhibitors of apoptosis protein; IAP; IAP binding peptide;

KW apoptosis induction; cytostatic; apoptosis; cancer; neuroblastoma;

KW intestine carcinoma; rectum carcinoma; colon carcinoma;

KW familial adenomatous polyposis carcinoma;
 KW hereditary non-polyposis colorectal cancer; oesophageal carcinoma;
 KW labial carcinoma; larynx carcinoma; hypopharynx carcinoma;
 KW tongue carcinoma; salivary gland carcinoma; gastric carcinoma;
 KW adenocarcinoma; medullary thyroidea carcinoma;
 KW paillary thyroidea carcinoma; renal carcinoma;
 KW kidney parenchyma carcinoma; ovarian carcinoma; cervix carcinoma;
 KW uterine corpus carcinoma; endometrium carcinoma; chorion carcinoma;
 KW pancreatic carcinoma; prostate carcinoma; testis carcinoma;
 KW breast carcinoma; urinary carcinoma; melanoma; brain tumour;
 KW glioblastoma; astrocytoma; meningioma; medulloblastoma;
 KW peripheral neuroectodermal tumour; Hodgkin lymphoma;
 KW non-Hodgkin lymphoma; Burkitt lymphoma; acute lymphatic leukaemia;
 KW chronic lymphatic leukaemia; acute myeloid leukaemia;
 KW chronic myeloid leukaemia; adult T-cell leukaemia lymphoma;
 KW hepatocellular carcinoma; gall bladder carcinoma; bronchial carcinoma;
 KW small cell lung carcinoma; non-small cell lung carcinoma;
 KW multiple myeloma; basalioma; teratoma; retinoblastoma;
 KW choroidea melanoma; seminoma; rhabdomyosarcoma; craniopharyngeoma;
 KW osteosarcoma; chondrosarcoma; myosarcoma; liposarcoma; fibrosarcoma;
 KW Ewing sarcoma; plasmocytoma.
 XX
 OS Synthetic.
 XX
 PN EP1378515-A1.
 XX
 PD 07-JAN-2004.
 XX
 PF 01-JUL-2002; 2002EP-00014074.
 XX
 PR 01-JUL-2002; 2002EP-00014074.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 PI Butz K, Crnkovic-Mertens I, Hoppe-Seyler F, Rausch C;
 XX
 DR WPI; 2004-073742/08.
 XX
 PT Novel peptide binding to inhibitors of apoptosis proteins and inducing
 PT apoptosis, useful for treatment of cancer.
 XX
 PS Claim 1; SEQ ID NO 81; 46pp; English.
 XX
 CC The present invention describes a peptide (I) which binds to inhibitors
 CC of apoptosis proteins (IAPs) and induces apoptosis, its fragment or
 CC derivatives. (I) has cytostatic activity, and can be used as an inducer
 CC of apoptosis. (I), optionally in combination with a active compound is
 CC useful for the manufacture of a medicament for the binding of IAPs, which
 CC are useful for treatment of cancer, where the cancer to be treated is
 CC chosen from the group consisting of neuroblastoma, intestine carcinoma,
 CC preferably rectum carcinoma, colon carcinoma, familial adenomatous
 CC polyposis carcinoma and hereditary non-polyposis colorectal cancer,
 CC oesophageal carcinoma, labial carcinoma, larynx carcinoma, hypopharynx
 CC carcinoma, tongue carcinoma, salivary gland carcinoma, gastric carcinoma,
 CC adenocarcinoma, medullary thyroidea carcinoma, paillary thyroidea
 CC carcinoma, renal carcinoma, kidney parenchyma carcinoma, ovarian
 CC carcinoma, cervix carcinoma, uterine corpus carcinoma, endometrium
 CC carcinoma, chorion carcinoma, pancreatic carcinoma, prostate carcinoma,
 CC testis carcinoma, breast carcinoma, urinary carcinoma, melanoma, brain
 CC tumours preferably glioblastoma, astrocytoma, meningioma, medulloblastoma
 CC and peripheral neuroectodermal tumours, Hodgkin lymphoma, non-Hodgkin
 CC lymphoma, Burkitt lymphoma, acute lymphatic leukaemia (ALL), chronic
 CC lymphatic leukaemia (CLL), acute myeloid leukaemia (AML), chronic myeloid
 CC leukaemia (CML), adult T-cell leukaemia lymphoma, hepatocellular
 CC carcinoma, gall bladder carcinoma, bronchial carcinoma, small cell lung
 CC carcinoma, non-small cell lung carcinoma, multiple myeloma, basalioma,
 CC teratoma, retinoblastoma, choroidea melanoma, seminoma, rhabdomyosarcoma,
 CC craniopharyngeoma, osteosarcoma, chondrosarcoma, myosarcoma, liposarcoma,
 CC fibrosarcoma, Ewing sarcoma and plasmocytoma. The present sequence
 CC represents a randomised peptide that binds to IAPs, which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 32 AA;

Query Match 47.5%; Score 75.5; DB 8; Length 32;
 Best Local Similarity 63.6%; Pred. No. 0.00028;

Matches 21; Conservative 1; Mismatches 10; Indels 1; Gaps 1;

```
Qy      1 GSRCIRRRISILFFVFRVLRSSRVLRSAEIIYES 33
      | : || || | ||| |||||
Db      1 GPSSLLRRCLILGMVLGVLR-RRVLRSAEIIYES 32
```

RESULT 3

ADH39939

ID ADH39939 standard; peptide; 34 AA.

XX

AC ADH39939;

XX

DT 25-MAR-2004 (first entry)

XX

DE Inhibitor of apoptosis protein (IAP) binding peptide SEQ ID NO:57.

XX

KW inhibitors of apoptosis protein; IAP; IAP binding peptide;
 KW apoptosis induction; cytostatic; apoptosis; cancer; neuroblastoma;
 KW intestine carcinoma; rectum carcinoma; colon carcinoma;
 KW familial adenomatous polyposis carcinoma;
 KW hereditary non-polyposis colorectal cancer; oesophageal carcinoma;
 KW labial carcinoma; larynx carcinoma; hypopharynx carcinoma;
 KW tongue carcinoma; salivary gland carcinoma; gastric carcinoma;
 KW adenocarcinoma; medullary thyroid carcinoma;
 KW papillary thyroid carcinoma; renal carcinoma;
 KW kidney parenchyma carcinoma; ovarian carcinoma; cervix carcinoma;
 KW uterine corpus carcinoma; endometrium carcinoma; chorion carcinoma;
 KW pancreatic carcinoma; prostate carcinoma; testis carcinoma;
 KW breast carcinoma; urinary carcinoma; melanoma; brain tumour;
 KW glioblastoma; astrocytoma; meningioma; medulloblastoma;
 KW peripheral neuroectodermal tumour; Hodgkin lymphoma;
 KW non-Hodgkin lymphoma; Burkitt lymphoma; acute lymphatic leukaemia;
 KW chronic lymphatic leukaemia; acute myeloid leukaemia;
 KW chronic myeloid leukaemia; adult T-cell leukaemia lymphoma;
 KW hepatocellular carcinoma; gall bladder carcinoma; bronchial carcinoma;
 KW small cell lung carcinoma; non-small cell lung carcinoma;
 KW multiple myeloma; basaloma; teratoma; retinoblastoma;
 KW chorioidea melanoma; seminoma; rhabdomyosarcoma; craniopharyngeoma;
 KW osteosarcoma; chondrosarcoma; myosarcoma; liposarcoma; fibrosarcoma;
 KW Ewing sarcoma; plasmocytoma.

XX

OS Synthetic.

XX

PN EP1378515-A1.

XX

PD 07-JAN-2004.

XX

PF 01-JUL-2002; 2002EP-00014074.

XX

PR 01-JUL-2002; 2002EP-00014074.

XX

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX

PI Butz K, Crnkovic-Mertens I, Hoppe-Seyler F, Rausch C;

XX

DR WPI; 2004-073742/08.

XX

PT Novel peptide binding to inhibitors of apoptosis proteins and inducing
 PT apoptosis, useful for treatment of cancer.

XX

PS Claim 1; SEQ ID NO 57; 46pp; English.

XX

CC The present invention describes a peptide (I) which binds to inhibitors
 CC of apoptosis proteins (IAPs) and induces apoptosis, its fragment or
 CC derivatives. (I) has cytostatic activity, and can be used as an inducer
 CC of apoptosis. (I), optionally in combination with a active compound is
 CC useful for the manufacture of a medicament for the binding of IAPs, which
 CC are useful for treatment of cancer, where the cancer to be treated is
 CC chosen from the group consisting of neuroblastoma, intestine carcinoma,
 CC preferably rectum carcinoma, colon carcinoma, familial adenomatous
 CC polyposis carcinoma and hereditary non-polyposis colorectal cancer,
 CC oesophageal carcinoma, labial carcinoma, larynx carcinoma, hypopharynx
 CC carcinoma, tongue carcinoma, salivary gland carcinoma, gastric carcinoma,
 CC adenocarcinoma, medullary thyroid carcinoma, papillary thyroid
 CC carcinoma, renal carcinoma, kidney parenchyma carcinoma, ovarian

SCORE Search Results Details for Application 10519539 and Search Result us-10-519-539-127.rai.

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OM protein - protein search, using sw model

Run on: August 17, 2006, 15:31:48 ; Search time 50 Seconds
(without alignments)
57.770 Million cell updates/sec

Title: US-10-519-539-127
Perfect score: 159
Sequence: 1 GSRCIRRRISILFFVFRVLRSSRVLRSAEIYES 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	54	34.0	248	2	US-09-902-540-15117	Sequence 15117, A
2	50	31.4	162	2	US-09-902-540-16022	Sequence 16022, A
3	48	30.2	350	2	US-09-107-532A-6978	Sequence 6978, Ap
4	48	30.2	626	2	US-09-949-016-8097	Sequence 8097, Ap
5	47	29.6	149	2	US-09-270-767-38074	Sequence 38074, A
6	47	29.6	149	2	US-09-270-767-53291	Sequence 53291, A
7	46.5	29.2	421	2	US-09-248-796A-18254	Sequence 18254, A
8	46.5	29.2	1912	2	US-09-495-714C-2	Sequence 2, Appli
9	46.5	29.2	1977	2	US-09-495-714C-4	Sequence 4, Appli
10	46.5	29.2	1985	2	US-09-495-714C-6	Sequence 6, Appli

11	46	28.9	216	2	US-09-270-767-56833	Sequence 56833, A
12	46	28.9	296	2	US-09-933-999A-35	Sequence 35, Appl
13	46	28.9	357	2	US-09-134-001C-4891	Sequence 4891, Ap
14	46	28.9	815	2	US-09-328-352-4284	Sequence 4284, Ap
15	45.5	28.6	1666	2	US-09-949-016-8322	Sequence 8322, Ap
16	45.5	28.6	1968	1	US-07-745-206A-7	Sequence 7, Appli
17	45.5	28.6	1968	1	US-08-455-543A-45	Sequence 45, Appl
18	45.5	28.6	1968	1	US-08-223-305C-45	Sequence 45, Appl
19	45.5	28.6	1968	1	US-08-311-363-7	Sequence 7, Appli
20	45.5	28.6	2161	1	US-07-745-206A-2	Sequence 2, Appli
21	45.5	28.6	2161	1	US-08-455-543A-49	Sequence 49, Appl
22	45.5	28.6	2161	1	US-08-455-543A-51	Sequence 51, Appl
23	45.5	28.6	2161	1	US-08-223-305C-49	Sequence 49, Appl
24	45.5	28.6	2161	1	US-08-223-305C-51	Sequence 51, Appl
25	45.5	28.6	2161	1	US-08-311-363-2	Sequence 2, Appli
26	45.5	28.6	2181	2	US-09-949-016-5981	Sequence 5981, Ap
27	45.5	28.6	2188	2	US-09-949-016-8295	Sequence 8295, Ap
28	45	28.3	60	2	US-09-134-001C-4624	Sequence 4624, Ap
29	45	28.3	189	2	US-09-252-991A-18166	Sequence 18166, A
30	45	28.3	865	2	US-09-612-204B-24	Sequence 24, Appl
31	45	28.3	865	2	US-10-055-364-24	Sequence 24, Appl
32	44.5	28.0	185	2	US-09-248-796A-21002	Sequence 21002, A
33	44	27.7	111	2	US-09-583-110-3344	Sequence 3344, Ap
34	44	27.7	149	2	US-09-270-767-45666	Sequence 45666, A
35	44	27.7	158	2	US-09-270-767-36587	Sequence 36587, A
36	44	27.7	158	2	US-09-270-767-51804	Sequence 51804, A
37	44	27.7	168	1	US-08-176-620A-10	Sequence 10, Appl
38	44	27.7	168	1	US-08-461-985-10	Sequence 10, Appl
39	44	27.7	168	2	US-08-932-787B-18	Sequence 18, Appl
40	44	27.7	168	2	US-08-932-012C-18	Sequence 18, Appl
41	44	27.7	168	2	US-08-888-818C-18	Sequence 18, Appl
42	44	27.7	232	2	US-09-489-039A-13233	Sequence 13233, A
43	44	27.7	676	2	US-09-270-767-44900	Sequence 44900, A
44	44	27.7	824	2	US-10-055-364-43	Sequence 43, Appl
45	44	27.7	874	2	US-08-804-439A-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-09-902-540-15117

; Sequence 15117, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 15117

; LENGTH: 248

; TYPE: PRT

; ORGANISM: Myxococcus xanthus

US-09-902-540-15117

Query Match 34.0%; Score 54; DB 2; Length 248;

Best Local Similarity 50.0%; Pred. No. 0.94;

Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GSR CIRRRISILFFVFRVLRSR 22

|| |: :|| || ||:

Db 77 GSAIPRKRLDVLFAVFAALRAR 98

RESULT 2

US-09-902-540-16022

; Sequence 16022, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

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; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16022
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16022
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Query Match          31.4%; Score 50; DB 2; Length 162;
Best Local Similarity 44.4%; Pred. No. 2.6;
Matches 16; Conservative 6; Mismatches 10; Indels 4; Gaps 2;
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Qy      2 SRCIRRRIS-ILFFVFRVL---RSRRVLRSAEIIYES 33
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Db      49 SDVIRQRVAGALFKPFALLYARARRVLATSEAYVS 84
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RESULT 3

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US-09-107-532A-6978
; Sequence 6978, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM:
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6978:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...350
; SEQUENCE DESCRIPTION: SEQ ID NO: 6978:
US-09-107-532A-6978
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Query Match 30.2%; Score 48; DB 2; Length 350;
Best Local Similarity 35.7%; Pred. No. 13;
Matches 10; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

RESULT 4

Query Match 30.2%; Score 48; DB 2; Length 626;
Best Local Similarity 69.2%; Pred. No. 26;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 5

Query Match 29.6%; Score 47; DB 2; Length 149;
Best Local Similarity 28.1%; Pred. No. 7.2;
Matches 9; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

RESULT 6

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; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53291
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-53291
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Query Match          29.6%; Score 47; DB 2; Length 149;
Best Local Similarity 28.1%; Pred. No. 7.2;
Matches    9; Conservative    14; Mismatches    5; Indels    4; Gaps    1;
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Qy      6 RRRISILFFVFRVLRSRRL----RSAEIIYES 33
        |: | :: || |: :||::| :::|:::
Db     11 RKNILLIAFVSRIGKSRKILVLTGKTSQIFQN 42
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RESULT 7

```
US-09-248-796A-18254
; Sequence 18254, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18254
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18254
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Query Match          29.2%; Score 46.5; DB 2; Length 421;
Best Local Similarity 38.2%; Pred. No. 29;
Matches   13; Conservative    8; Mismatches   12; Indels    1; Gaps    1;
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        || |: | | : : |: ::|: ||| | :|
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RESULT 8

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US-09-495-714C-2
; Sequence 2, Application US/09495714C
; Patent No. 6670465
; GENERAL INFORMATION:
; APPLICANT: University Technologies International Inc.
; TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) 1F-SUBUNIT GENE
; FILE REFERENCE: 45499.4 (formerly 45074.6)
; CURRENT APPLICATION NUMBER: US/09/495,714C
; CURRENT FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1912
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-495-714C-2
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Query Match          29.2%; Score 46.5; DB 2; Length 1912;
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